

TABLE S1. The C-terminal 10 amino acids of (A) 37 *E. coli* MG1655 OMP β barrels (B) 80 predicted trimeric porins that mediate carbohydrate uptake in Gammaproteobacteria and (C) 20 predicted *E. coli* FimD family proteins.

A

#	Protein	Sequence ID	C-terminal 10 amino acids of β barrel
1	Ag43	YP_026164.1	NGQATLNVT
2	BamA ^a	NP_414719.1	RMSAGIALQW
3	BcsC	YP_026226.4	HFLLYVRYSA
4	BtuB	NP_418401.1	EYTLSGSYTF
5	CirA	NP_416660.1	RYFMAVDYRF
6	FadL	NP_416846.2	AWLFGTNFNY
7	FecA	NP_418711.1	TLYMQGSLKF
8	FepA	NP_415116.1	TWYMSVNTHF
9	Fhua	NP_414692.1	QVVATATFRF
10	FhuE	NP_415620.1	NFSITGTYQF
11	Fiu	NP_415326.1	TFLLTANMHF
12	LptD	NP_414596.1	AVYDNAIGFN
13	MipA	NP_416296.1	LISTGITYKF
14	NanC	NP_418731.2	SYRIGVSFKL
15	OmpA	NP_415477.1	MLSLGVSYRF
16	OmpC	NP_416719.1	IVALGLVYQF
17	OmpF	NP_415449.1	TVAVGIVYQF
18	OmpG	NP_415835.1	YAGVGVNYSF
19	OmpL	NP_418311.1	QIRIGTKYFF
20	OmpN	NP_415895.1	IVALGLVYQF
21	OmpT	NP_415097.1	ITTAGLKTYTF
22	OmpW	NP_415772.1	VFMFSAGYRF
23	OmpX	NP_415335.1	TWIAGVGYRF
24	PagP	NP_415155.1	VYFAWMRFQF
25	PgaA	NP_415543.1	YVEFDMDTFRF
26	PhoE	NP_414776.1	IVAVGMTYQF
27	PldA	NP_418265.1	NQTRVGVGVM
28	TamA ^b	NP_418641.1	KTGTGVGVRW
29	Tsx	NP_414945.1	GGYLVVGYNF
30	YaiO	NP_414892.1	QLAARLTWKF
31	YddB	NP_416012.1	TFWLDVSMKF
32	YfaZ	NP_416753.4	GPYVGVNASF
33	YfeN	NP_416903.1	AIISIKFNF
34	YhjY	NP_418004.4	LYTMGV SARF
35	YncD	NP_415968.1	GVGMNIAWRF
36	YpjA	NP_417134.2	NAVAGVNWSF
37	YsaC	NP_418041.1	TFVTGVSWRF

B

#	Strain	Sequence ID	C-terminal 10 amino acids of β barrel ^c	Sequence identity to LamB ^d
1	<i>Escherichia coli</i> str. K-12 substr. MG1655	LamB (NP_418460.1)	TFGAQMEIWW	--
2	<i>Escherichia coli</i> str. K-12 substr. MG1655	BglH (NP_418176.1)	AVGAQAEIWW	26%
3	<i>Acinetobacter baumannii</i>	WP_057048239.1	NFGLQVEYWW	29%
4	<i>Acinetobacter bereziniae</i>	ATZ62059.1	NFGIQLENWW	29%
5	<i>Acinetobacter calcoaceticus</i>	WP_045432189.1	NFGIQYEYWW	29%
6	<i>Acinetobacter oleivorans</i>	KHN66258.1	NFGVQLEYWW	31%
7	<i>Acinetobacter pittii</i>	OCY43804.1	NFGMQLEYWW	30%
8	<i>Acinetobacter pittii</i> ANC 4050	EOQ71221.1	NFGVQLEHWW	31%
9	<i>Acinetobacter</i> sp. ANC 4558	WP_086181506	NFGVQIEYWW	28%
10	<i>Acinetobacter</i> sp. MB5	WP_111895452.1	NFGLQIEYWW	28%
11	<i>Acinetobacter</i> sp. Root1280	KQX00275.1	NFGAQLEYWW	31%
12	<i>Actinobacillus succinogenes</i>	WP_011978975.1	VAGVQFEAWW	55%
13	<i>Aeromonas hydrophila</i>	AKA18444.1	QVGVQAEAWW	38%
14	<i>Aeromonas salmonicida</i>	WP_011898996.1	NFGVQAEAWW	39%
15	<i>Algicola sagamiensis</i>	WP_018692859.1	TLGIQVESWW	27%
16	<i>Alkalilimnicola ehrlichii</i>	WP_116348444.1	TFGLQTEVWW	37%
17	<i>Aquisalimonas asiatica</i>	WP_091640571.1	SVGAQVETWW	31%
18	<i>Azoarcus</i> sp. KH32C	WP_015436292.1	LVGAQMEVWF	25%
19	<i>Betaproteobacteria bacterium</i>	TAH46134.1	LMGAQMEVWF	25%
20	<i>Burkholderia ubonensis</i>	KVA21652.1	SIGAQAEVWW	27%
21	<i>Candidatus Thiodictyon syntrophicum</i>	AUB79554.1	TFGAQVEAWW	40%
22	<i>Corallincola</i>	WP_114337853.1	RFGAQVEAWW	36%
23	<i>Cricetibacter osteomyelitidis</i>	WP_131977784.1	IVGVQMEAWW	58%
24	<i>Cricetibacter osteomyelitidis</i>	WP_131977784.1	IVGVQMEAWW	58%
25	<i>Escherichia coli</i>	WP_032488482.1	NFGVQMETWF	26%
26	<i>Glaesserella</i> sp. 15-184	AUI66399.1	IGGVQFEAWW	53%
27	<i>Idiomarina</i> sp. H105	KTG24878.1	TFGVQTEVWF	22%
28	<i>Iodobacter fluviatilis</i>	WP_130104888.1	TFGAQAEVWW	39%
29	<i>Janthinobacterium</i>	WP_070218107.1	SFGLQVETWF	29%
30	<i>Janthinobacterium</i> sp. 1_2014MBL_MicDiv	WP_071324311.1	TVGVQVESWW	37%
31	<i>Mannheimia granulomatis</i>	EXI63060.1	ITGVQFEAWW	52%
32	<i>Marinobacter aromaticivorans</i>	WP_100688099.1	TFGTQMEIWF	27%
33	<i>Marinobacter fuscus</i>	WP_106760835.1	RVGAQVEAWW	87%
34	<i>Marinobacter hydrocarbonoclasticus</i>	HCP21192.1	QLGAQIEAWW	37%
35	<i>Marinobacter lipolyticus</i>	WP_012136733.1	TFGTQMEVWF	26%
36	<i>Marinobacter shengliensis</i>	WP_106695496.1	QIGAQIEAWW	36%
37	<i>Marinobacter</i> sp. YJ-S3-2	TBW54425.1	QLGVQMEAWW	39%
38	<i>Marinobacter</i> sp. YJ-S3-2	TBW51267.1	TFGVQAETWF	28%
39	<i>Marinobacter subterrani</i>	WP_048494981.1	QVGAQIEAWW	37%
40	<i>Marinobacterium lutimaris</i>	WP_104003022.1	TVGLQVEYSW	28%
41	<i>Marinomonas</i> sp. QM202	WP_087612095.1	TVGARFEAWF	25%
42	<i>Marinomonas spartinae</i>	WP_067018547.1	LFALQMETWF	23%
43	<i>Marinomonas spartinae</i>	SBS35014.1	LFALQMETWF	23%
44	<i>Massilia plicata</i>	WP_134385470.1	SYGVQLEAWW	30%
45	<i>Motiliiproteus</i> sp. MSK22-1	WP_076720703.1	TYGVQMEAWW	50%

46	<i>Oceanobacter kriegii</i>	WP_051219364.1	SFGAQTEVWF	38%
47	<i>Oceanobacter kriegii</i>	WP_051219017.1	SFGVQAEVWW	38%
48	<i>Otariodibacter oris</i>	RKR72714.1	IGGIQMEAWW	54%
49	<i>Pasteurella multocida</i>	WP_126374016.1	IYGVQFEAWW	53%
50	<i>Pasteurellaceae bacterium</i>	OOF52399.1	IAGVQFEAWW	53%
51	<i>Pseudoalteromonas haloplanktis TAC125</i>	CAI89260.1	VAGAQVEIWF	27%
52	<i>Pseudoalteromonas translucida KMM 520</i>	ALS34835.1	VAGAQVEVWF	27%
53	<i>Pseudogulbenkiania sp. MAI-1</i>	WP_024302059.1	TIGAQAEAWW	39%
54	<i>Pseudomonas brassicacearum</i>	WP_025212027.1	NVGVQVEYWW	33%
55	<i>Pseudomonas silesiensis</i>	WP_064679286.1	QYGIQMETWF	25%
56	<i>Pseudomonas sp. PIC25</i>	WP_095598843.1	QFGVQMETWF	23%
57	<i>Pseudomonas sp. TTU2014-066ASC</i>	WP_058078226.1	TFGVQAEAWW	61%
58	<i>Psychromonas aquimarina</i>	WP_028865990.1	IAGMQMETWF	24%
59	<i>Psychromonas arctica</i>	WP_028870109.1	QFGVQAEAWW	40%
60	<i>Psychromonas hadalis</i>	WP_022941929.1	SLGVQMEAWW	36%
61	<i>Psychromonas ossibalaenae</i>	WP_019614444.1	NFGVQMEAWW	37%
62	<i>Psychromonas ossibalaenae</i>	WP_019614266.1	VAGMQMETWF	24%
63	<i>Psychromonas ossibalaenae</i>	WP_019615795.1	SVGMQAEAWW	34%
64	<i>Psychromonas sp. psych-6C06</i>	WP_101108148.1	NFGIQAEAWF	35%
65	<i>Reinekea marinisedimentorum</i>	WP_132701207.1	TLGAMFEAWW	23%
66	<i>Rhizobacter sp. Root1221</i>	WP_056670936.1	RYGVQAEVWW	28%
67	<i>Rivibacter sp. C1-9</i>	WP_140635602.1	TYGVQAEVWW	37%
68	<i>Shewanella sp. SNU WT4</i>	WP_140932889.1	IFGAQVETWF	25%
69	<i>Shewanella violacea DSS12</i>	BAJ03734.1	STGIQVETWW	28%
70	<i>Testudinibacter aquarius</i>	WP_132968018.1	VYGVQFEAWW	56%
71	<i>Thauera sp. 27</i>	WP_002945077.1	LLGAQMEVWF	26%
72	<i>Vibrio diazotrophicus</i>	WP_102965680.1	SFGVQAEIWW	24%
73	<i>Vibrio fluvialis</i>	WP_032079918.1	IFALQMETWF	26%
74	<i>Vibrio fluvialis</i>	WP_020428838.1	AFALQMETWF	27%
75	<i>Vibrio mangrovi</i>	WP_087481112.1	TFGVQAEVWW	26%
76	<i>Vibrio natriegens</i>	WP_065298323.1	SFGVQADIWW	25%
77	<i>Vibrio parahaemolyticus</i>	KKF71314.1	SFGAQMEIWW	79%
78	<i>Vibrio sp. E4404</i>	WP_109320058.1	SAGVQVELFW	24%
79	<i>Vibrio sp. H11</i>	WP_136483121.1	VFALQMETWF	25%
80	<i>Vibrio tritonius</i>	WP_068711623.1	SFGVQAEIWW	25%

C

#	Protein	<i>E. coli</i> strain	Protein sequence ID	C-terminal 10 amino acids of β barrel	Sequence identity to FimD β barrel ^e	β barrel location ^f
1	FimD	MG1655	NP_418737.1	YGVSGGVLAH	--	184-704
2	ElfC	MG1655	NP_415460.1	YALSGSLVAH	49%	174-694
3	HtrE	MG1655	NP_414681.1	LSTDGGFVLH	33%	176-696
4	SfmD	MG1655	NP_415065.1	WQLSGGVVGH	47%	179-699
5	YbgQ	MG1655	NP_415246.2	SSWSGSFTAT	34%	155-675
6	YehB	MG1655	NP_416612.1	ASVSGGIVAW	31%	153-673
7	YhcD	MG1655	NP_417683.1	GTMSGGIAVH	32%	152-672
8	YqiG	MG1655	AIZ89931.1	ASWNGSFTAT	31%	156-676
9	YraJ	MG1655	AAA57947.1	YGVTTGGVVIH	39%	182-702
10	AfaC	3431	EFU95499.1	AGMSGSMVAH	34%	185-705
11	AM465_17900	JJ1886	AGY84370.1	YGMGGIIAH	62%	186-706
12	CS3-2	2871950	EMV63731.1	GGIEGGILVY	30%	80-600
13	CssD	2845350	EMW26396.1	YSASGGIVLH	23%	158-678
14	FanD	B41	EIJ05038.1	AQIGGAIIGV	28%	158-678
15	FasD	N/A	WP_063079412.1	YSLSGSAILY	31%	159-679
16	FocD	H461	OSL47508.1	YGLSGGILAH	67%	185-705
17	LpfC	O26	EAB0635723.1	YGVVRGGIVVH	46%	179-699
18	PapC	J96	ELL39279.1	VSASGGATIT	33%	172-692
19	SfpC	O177	TVM36184.1	MSASGGATIT	34%	178-698
20	YfcU	UMNF18	AEJ57557.1	LSLQGGATLT	32%	171-691

^a The BamA β-signal has been shown to locate in β-strand 14 (C. L. Hagan, J. S. Wzorek, and D. Kahne, Proc Natl Acad Sci USA 112(7):2011–2016, 2015, doi:10.1073/pnas.1415955112).

^b Based on the homology and structural similarity of TamA to BamA, its β-signal is likely located in β-strand 14 (F. Gruss, F. Zähringer, R. P. Jakob, B. M. Burmann, S. Hiller, and T. Maier, Nat Struct Mol Biol 20(11):1318-20, 2013, doi: 10.1038/nsmb.2689).

^c The C-terminus was identified by alignment to *E. coli* MG1655 LamB (R. Dutzler, Y. F. Wang, P. Rizkallah, J. P. Rosenbusch, and T. Schirmer, Structure 4(2):127-134, 1996, doi:10.1016/s0969-2126(96)00016-0).

^d The sequence identity is based on the alignment of the complete protein sequence to LamB.

^e The location of the *E. coli* MG1655 FimD β barrel was previously determined by x-ray crystallography (PDB 3RFZ) (G. Phan, H. Remaut, T. Wang, et al., Nature 474(7349):49-53, 2011, doi:10.1038/nature10109).

^f The location of the β barrel is based on alignment of the protein sequence with the sequence of FimD.